

SEQ. ID 3-1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTGAAGGATCT 60  
 SEQ. ID 4-1 M T F N S F E G S 9

61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGAATTTGTAGAAGAGTTTAATAGA 120  
 10 K T C V P A D I N K E E E F V E E F N R 29

121 TTAAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCAACACTGGCACGA 180  
 30 L K T F A N F P S G S P V S A S T L A R 49

181 GCAGGGTTTCTTTATACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTCATGCAGCT 240  
 50 A G F L Y T G E G D T V R C F S C H A A 69

241 GTAGATAGATGGCAATATGGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCAAAT 300  
 70 V D R W Q Y G D S A V G R H R K V S P N 89

301 TGCAGATTTATCAACGGCTTTTATCTTGAAAATAGTGCCACGCAGTCTACAAATTCTGGT 360  
 90 C R F I N G F Y L E N S A T Q S T N S G 109

361 ATCCAGAATGGTCAGTACAAAGTTGAAAATCTCTGGAAGCAGAGATCATTTCGCCTTA 420  
 110 I Q N G Q Y K V E N Y L G S R D H F A L 129

421 GACAGGCCATCTGAGACACATGCAGACTATCTTTGAGAACTGGGCAGGTTGTAGATATA 480  
 130 D R P S E T H A D Y L L R T G Q V V D I 149

481 TCAGACACCATATACCCGAGGAACCCTGCCATGTATaGTGAAGAAGCTAGATTAAAGTCC 540  
 150 S D T I Y P R N P A M Y S E E A R L K S 169

541 TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTGCTGGACTC 600  
 170 F Q N W P D Y A H L T P R E L A S A G L 189

601 TACTACACAGGTATTGGTGACCAAGTGCAGTGCTTTTGTGTGGTGGAAAATGAAAAT 660  
 190 Y Y T G I G D Q V Q C F C C G G K L K N 209

661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGCGACACTTTCCTAATTGCTTCTTT 720  
 210 W E P C D R A W S E H R R H F P N C F F 229

721 GTTTTGGGCCGAATCTTAATATTGCAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT 780  
 230 V L G R N L N I R S E S D A V S S D R N 249

781 TTCCCAAATTCAACAAATCTTCCAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC 840  
 250 F P N S T N L P R N P S M A D Y E A R I 269

841 TTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTT 900  
 270 F T F G T W I Y S V N K E Q L A R A G F 289

901 TATGCTTTAG<sup>1,2</sup>GTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGAGGGCTAACTGAT 960  
 290 Y A L G E G D K V K C F H C G G G L T D 309

961 TGGAAGCCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGG<sup>2,3</sup>GTGCAAATAT 1020  
 310 W K P S E D P W E Q H A K W Y P G C K Y 329

1021 CTGTTAGAACAGAAGGGACAAGAATATATAAACAATATTCATTAACTCATTCACTTGAG 1080  
 330 L L E Q K G Q E Y I N N I H L T H S L E 349

Fig. 1

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**Fig. 1 (cont.)**

3061 AATATTGGCAAGAAAAGAAGAATAGTTGTTTAAATATTTTTTAAAAAACACTTGAATAAG 3120  
 3121 AATCAGTAGGGTATAAACTAGAGTTTAAAAATGCCTCATAGAACGTCCAGGGTTTACAT 3180  
 3181 TACAAGATTCTCACAACAAACCCATTGTAGAGGTGAGTAAGGCATGTTACTACAGAGGAA 3240  
 3241 AGTTTGAGAGTAAACTGTAAAAAATTATATTTTTGTTGTACTTTCTAAGAGAAAAGAGTA 3300  
 3301 TTGTTATGTTCTCCTAACTTCTGTTGATTACTACTTTAAGTGATATTCATTTAAACATT 3360  
 3361 GCAAATTTATTTTATTTTATTTTAAATTTCTTTTGTAGATGGAGTCTTGCTTGTCACCCAGG 3420  
 3421 CTGGAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCCTTCTGGGTTCAAGCGAT 3480  
 3481 TCTCGTGCCTCAGCTTCTGAGTAGCTGGAATTACAGGCAGGTGCCACCATGCCCGACTA 3540  
 3541 ATTTTTTTTTATTTTATTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTATCAAAC 3600  
 3601 TCCTGACCTCAAGAGATCCACTCGCCTTGCCCTCCCAAAGTGCTGGGATTACAGGCTTGA 3660  
 3661 GCCACCACGCCCGCTAAACATTGCAAATTTAAATGAGAGTTTTAAAAATTAAATAATG 3720  
 3721 ACTGCCCTGTTTCTGTTTTAGTATGTAAATCCTCAGTCTTACCTTTGCACTGTCTGCC 3780  
 3781 ACTTAGTTGGTTATATAGTCATTAACCTGAATTTGGTCTGTATAGTCTAGACTTTAAAT 3840  
 3841 TTAAAGTTTCTACAAGGGGAGAAAAGTGTTAAATTTTAAATATGTTTCCAGGACA 3900  
 3901 CTTCACTTCCAAGTCAGGTAGGTAGTTCAATCTAGTTGTTAGCCAAGGACTCAAGGACTG 3960  
 3961 AATTGTTTAAACATAAGGCTTTTCTGTTCTGGGAGCCGCACTTCATTAATAATTCTTCTA 4020  
 4021 AAACCTGTATGTTTAGAGTTAAGCAAGACTTTTTTCTTCTCCTCTCCATGAGTTGTGAAAT 4080  
 4081 TTAATGCACAACGCTGATGTGGCTAACAAGTTTATTTTAAAGATTGTTTAGAAATGCTGT 4140  
 4141 TGCTTCAGGTTCTTAAATCACTCAGCACTCCAACCTTAATCAAATTTTGGAGACTTA 4200  
 4201 ACAGCATTTGTCTGTGTTTGAACATAAAAAGCACCGGATCTTTCCATCTAATTCGCA 4260  
 4261 AAAATTGATCATTTGCAAAGTCAAAACTATAGCCATATCCAAATCTTTCCCCCTCCCAA 4320  
 4321 GAGTTCTCAGTGTCTACATGTAGACTATTCCTTTTCTGTATAAAGTTCACTCTAGGATTT 4380  
 4381 CAAGTCACCACTTATTTTACATTTTAGTCATGCAAAGATTCAAGTAGTTTGCATAAGT 4440  
 4441 ACTTATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAGCATTGTCTTAATTTTGGAG 4500  
 4501 AACTGGTTTTAGCATTTACAACTAAATTCAGTTAATTAATTAATAGCTTTATATTGCC 4560  
 4561 TTTCTGCTACATTTGGTTTTTCCCCTGTCCCTTTGATTACGGGCTAAGGTAGGGTAAG 4620  
 4621 AXXGGGTGTAGTGAGTGTATATAATGTGATTTGGCCCTGTGTATTATGATATTTGTTAT 4680  
 4681 TTTTGTGTTATATTATTTACATTTTCTAGTGTGTTTTTGTGTTTCCATTTTAGGGGAT 4740  
 4741 AAAATTTGTATTTTGAACATATGAATGGAGACTACCGCCCCAGCATTAGTTTCACATGATA 4800  
 4801 TACCCTTTAAACCCGAATCATTGTTTTATTTCTGATTACACAGGTGTTGAATGGGGAAA 4860  
 4861 GGGGCTAGTATATCAGTAGGATATACTATGGGATGTATATATATCATTGCTGTTAGAGAA 4920  
 4921 ATGAAATAAATGGGGCTGGGCTCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGG 4980  
 4981 CTGAGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC 5040  
 5041 CCCGTCTCTACTAAAAACAGAAAATTAGCCGGCGTGGTGGCGGGCGCCTGTAGTCCCA 5100  
 5101 GCTACTCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCAGAGCTTGCACTGA 5160  
 5161 GCCGAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAA 5220  
 5221 AAAAAAAAAAAG 5232

Fig. 1 (cont.)

SEQ. ID 5-1 T T G C T C T G T C A C C C A G T T T G G A G T G C A G T T A T G C A G T C T C A C A C T G C A A G C T C T G C C T C A 60  
61 T G G G C T C A A G T G A A C C T C C T G C C T C A G C C T C T C A A G T A G C T G G G A C C A C A G G C A G G T G C C 120  
121 A C C A T G T C T G G C T A A T T T T T G A G T T T C T T T G T A G A G A T G G T G T T T T G C C A A G T C A C C C A G 180  
181 T T T G A G G C T G G T C T C A A A C A C C T G G G C T C A A G C A A T C C A T C T A C C T C A G C C T C C C A A A G T 240  
241 G C T G G G A T T A C A G G A G T G A G C C A T G G C A T G A G G C C T T G T G G G G T G T C T C T T T T A A A T G A A 300  
301 A G C A T A C T C T G T T T A C G T A T T T G A T A T G A A G G A A T A T C C T T C C T T T C C A C A A A G A C A A A A 360  
361 A T T A T C C T A T T T T T C T C A A A A C A T A T G T C C T T T T T C T C T A C T T T T C A T T T T T G T T A C T T T 420  
421 T G A T G G A C A C A T G T G T T A C A T T G A T T T C A C T T T C T C A T A A T T C T G C T G T A A G A A A A C A A 480  
481 T A G T G C C A G T T C A A T G A C A A A T A G C A A C A G T C T G T T A T T G C T A G A C T G T T A C T G T T A G T G 540  
541 G A G A C T A C C A G A A C A G T C A G T C C C A G T G T C A G G G A A T C A A A G A G A A C A T G T T C C C T C T C T 600  
601 A A A G G G C A C A G C T G C T G C T C A G C T T T A G C T A G T T G C T G C C C T G C A G G A C T A T A G G C C C A G 660  
661 T G T T G C T A G A T C T T T T G A T G T T T C A A G A G A A G C T T G G A A T C T A G A A T G T G A T G G G A A G T C 720  
721 T C T T A C A T T T A A A C A T G T T G G C A A T T A A T G G T A A G A T T T A A A A A T A C T G T G G T C C A A G A A 780  
781 A A A A A T G G A T T T G G A A A C T G G A T T A A A T T C A A A T G A G G C A T G C A G A T T A A T C T A C A G C A T 840  
841 G G T A C A A T G T G A A T T T T C T G G T T C T T A A T T G C A C T G T A A T T A G G T A A G A T G T T A G C T T 900  
901 T G G G G A A G C T A A G T G C A G A T A T G C A G A A A C T A T T A T T T T T G T A A G T T T T C T C T A A G T A T 960  
961 A A A T A A A T T T C A A A A T A A A A A T A A A A A C T T A G T A A A G A A C T A T A A T G C A A T T C T A T G T A A 1020  
1021 G C C A A A C A T A A T A T G T C T T C C A G T T T G A A A C C T C T G G G T T T T A T T T T A T T T T A T T T T A T T 1080  
1081 T T T G A G A C A G A G T C T T G C T G T G T C A C C C A G G C T G G A G T G T A G T G G C A C T A T T T C G G C C C A 1140  
1141 C T G C A A C C T C C A C C T C C C A G G C T C A A A T G A T T C T C C T G C C T C A G C C T C C G G A G T A G C T G G 1200  
1201 G A T T A C A G G C G C G T A C C A C C A C C C A G C T A A T T T T T G T A T T T T A G T A G A G A T G G G G T T 1260  
1261 T C A C C A T T T T G G C C A G G C T G G T T T T G A A C C C T G A C C T C A A G T G A T C C A C T T G T C T T G G C 1320  
1321 C T C C C A A A A T G C T G G G A T T A C A G G C G T G A G C C A C T G C A C C A G G C A G A G G C C T C T G T T T T T 1380  
1381 T A T C T C T T T T T G G C C T C T A C A G T G C C T A G T A A A G C A C C T G A T A C A T G G T A A A C G A T C A G T 1440  
1441 A A T T A C T A G T A C T C T A T T T T G G A G A A A T G A T T T T T A A A A A G T C A T T G T G T T C C A T C C A 1500  
1501 T G A G T C G T T T G A G T T T T A A A A C T G T C T T T T G T T T G T T T T T G A A C A G G T T T A C A A G G A G 1560  
1561 G A A A A C G A C T T C T T C T A G A T T T T T T T C A G T T T C T T A T A A A T C A A A A C A T C T C A A A A 1620  
1621 T G G A G A C C T A A A A T C C T T A A G G G A C T T A G T C T A A T C T C G G G A G G T A G T T T T G T G C A T G G 1680  
1681 G T A A A C A A A T T A A G T A T T A A C T G G T G T T T A C T A T C C A A A G A A T G C T A A T T T T A T A A A C A 1740  
1741 T G A T C G A G T T A T A T A A G G T A T A C C A T A A T G A G T T T G A T T T T G A A T T T G A T T T G T G G A A A T 1800  
1801 A A A G G A A A A G T A T T C T A G C T G G G G C A T A T T G T T A A A G C A T T T T T T C A G A G T T G G C C A G 1860  
1861 G C A G T C T C C T A C T G G C A C A T T C T C C C A T T A T G T A G A A T A G A A A T A G T A C C T G T G T T T G G G 1920  
1921 A A A G A T T T T A A A A T G A G T G A C A G T T A T T T G G A A C A A A G A G C T A A A T A A T C A A T C C A C T G C A 1980  
1981 A A T T A A A G A A A C A T G C A G A T G A A A G T T T T G A C A C A T T A A A A T A C T T C T A C A G T G A C A A A G 2040  
2041 A A A A A T C A A G A C A A A G C T T T T T G A T A T G T G C A A C A A A T T A G A G G A A G T A A A A A G A T A A 2100  
2101 A T G T G A T G A T T G G T C A A G A A A T T A C C A G T T A T T A C A A G G C C A C T G A T A T T T T A A A C G T 2160  
2161 C C A A A A G T T T G T T T A A A T G G G C T G T T A C C G T G A G A A T G A T G A G G A T G A G A A T G A T G G T T 2220  
2221 G A A G G T T A C A T T T T A G G A A A T G A G A A A C T T A G A A A A T T A A T A T A A A G A C A G T G A T G A A T 2280  
2281 A C A A G A A G A T T T T T A T A A C A A T G T G T A A A A T T T T T G G C C A G G G A A A G G A A T A T T G A A G T 2340  
2341 T A G A T A C A A T T A C T T A C C T T T G A G G G A A A T A A T T G T T G G T A A T G A G A T G T G A T G T T T C T C 2400  
2401 C T G C C A C C T G G A A A C A A A G C A T T G A A G T C T G C A G T T G A A A A G C C C A C G T C T G T G A G A T C 2460  
2461 C A G G A A A C C A T G C T T G C A A A C C A C T G G T A 2520  
2521 T G A C T T G C T T A T T G G T C A T T G C T A G T A T T A T C G A C T C A G A A C C T C T T T A C T A A T G G C T A G 2580  
2581 T A A A T C A A A T T G A G A A A T T C T G A A T T T T G A C A A G G T C T C T G C T G T T G A A A T G G T A A A T T 2640  
2641 T A T T A T T T T T T T G T C A T G A T A A A T T C T G G T T C A A G G T A T G C T A T C C A T G A A A T A A T T T C 2700  
2701 T G A C C A A A C T A A A T T G A T G C A A T T T G A T T A T C C A T C T T A G C C T A C A G A T G G C A T C T G G T 2760  
2761 A A C T T T T G A C T G T T T T A A A A A T A A A T C C A C T A T C A G A G T A G A T T T G A T G T T G G C T T C A G 2820  
2821 A A A C A T T T A G A A A A C A A A A G T T C A A A A T G T T T T C A G G A G G T G A A A G T T G A A T A A C T C 2880  
2881 T A C A A T G T T A G T T C T T T G A G G G G A C A R A A A A T T T A A A T C T T T G A A A G G T C T T A T T T T A 2940  
2941 C A G C C A T A T C T A A A T T A T C T T A A G A A A A T T T T A C A A A G G G A A T G A A A T A T A T A T A T C A T G 3000  
3001 A T T C T G T T T T T C C A A A A G T A A C C T G A A T A T A G C A A T G A A G T T C A G T T T T G T T A T T G G T A G 3060  
3061 T T T G G G C A G A G T C T C T T T T T G C A G C A C C T G T T G T C T A C C A T A A T T A C A G A G G A C A T T T C C 3120  
3121 A T G T T C T A G C C A A G T A T A C T A T T A G A A T A A A R A A A C T T A A C A T T G A G T T G C T T C A A C A G C 3180

Fig. 2

3181 ATGAACTGAGTCCAAAAGACCAAATGAACAAACACATTAATCTCTGATTATTTATTTTA 3240  
 3241 AATAGAATATTTAATTGTGTAAGATCTAATAGTATCATTATACTTAAGCAATCATATTCC 3300  
 3301 TGATGATCTATGGGAAATAACTATTATTTAATTAATATTGAAACCAGGTTTAAAGATGTG 3360  
 3361 TTAGCCAGTCCTGTTACTAGTAAATCTCTTTATTTGGAGAGAAATTTTAGATTGTTTGT 3420  
 3421 TCTCCTTATTAGAAGGATTGTAGAAAGAAAAAATGACTAATTGGAGAAAAATTGGGGAT 3480  
 3481 ATATCATATTTCACTGAATTCAAAATGTCTTCAGTTGTAAATCTTACCATTATTTACGT 3540  
 3541 ACCTCTAAGAAATAAAAGTGCTTCTAATTAATAATATGATGTCATTAATTATGAAATACTT 3600  
 3601 CTTGATAACAGAAGTTTTAAATAGCCATCTTAGAATCAGTGAAATATGGTAATGTATTA 3660  
 3661 TTTTCCTCCTTTGAGTNAGGTCTGTGCTTTTTNTTCCTGGCCACTAAATNTCACCATNT 3720  
 3721 CCAANAAGCAAANTAAACCTATTCTGAATATTTTGTGCTGTGAAACACTTGNCAGCAGAGC 3780  
 3781 TTTCCCNCCATGNNAGAAGCTTCATGAGTCACACATTACATCTTTGGGTGATTGAATGC 3840  
 3841 CACTGAAACATTTCTAGTAGCCTGGAGNAGTTGACCTACCTGTGGAGATGCCCTGCCATTA 3900  
 3901 AATGGCATCCTGATGGCTTAATACACATCACTCTTCTGTGNAGGGTTTTAATTTCAACA 3960  
 3961 CAGCTTACTCTGTAGCATCATGTTTACATTGTATGTATAAAGATTATACNAAGGTGCAAT 4020  
 4021 TGTGTATTTCTTCTTAAATGTATCAGTATAGGATTTAGAATCTCCATGTTGAAACTCT 4080  
 4081 AAATGCATAGAAATAAAAAATAATAAAAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTA 4140  
 4141 AAATGATAAAAGCAAAGCCATGCACAAAACCTACCTCCCTAGAGAAAGGCTAGTCCCTTT 4200  
 4201 TCTTCCCCATTCAATTCATTATGAACATAGTAGAAAACAGCATATTCTTATCAAATTTGA 4260  
 SEQ. ID 6-1 M N I V E N S I F L S N L M 14  
 4261 TGAAAAGCGCCAACACGTTTGAACGTGAAATACGACTTGTCATGTGAACGTGACCGAATGT 4320  
 15 K S A N T F E L K Y D L S C E L Y R M S 34  
 4321 CTACGTATTCCACTTTTCTGCTGGGGTTCCTGTCTCAGAAAGGAGTCTTGCTCGTGCTG 4380  
 35 T Y S T F P A G V P V S E R S L A R A G 54  
 4381 GTTCTATTACACTGGTGTGAATGACAAGGTCAAATGCTTCTGTTGTGGCCTGATGCTGG 4440  
 55 F Y Y T G V N D K V K C F C C G L M L D 74  
 4441 ATAACGTGAAAAAGAGGAGACAGTCCTACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCA 4500  
 75 N W K R G D S P T E K H K K L Y P S C R 94  
 4501 GATTCGTTCCAGAGTCTAAATTCGGTTAACAACCTGGAAGCTACCTCTCAGCCTACTTTTC 4560  
 95 F V Q S L N S V N N L E A T S Q P T F P 114  
 4561 CTTCTTCAGTAACACATTCCACACACTCATTACTTCCGGGTACAGAAAACAGTGGATATT 4620  
 115 S S V T H S T H S L L P G T E N S G Y F 134  
 4621 TCCGTGGCTCTTATTCAAACCTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGAAT 4680  
 135 R G S Y S N S P S N P V N S R A N Q E F 154  
 4681 TTTCTGCCTTGATGAGAAGTTCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTAC 4740  
 155 S A L M R S S Y P C P M N N E N A R L L 174  
 4741 TTACTTTTCAGACATGGCCATTGACTTTTCTGTGCGCCAACAGATCTGGCAGCAGCAGGCT 4800  
 175 T F Q T W P L T F L S P T D L A R A G F 194  
 4801 TTTACTACATAGGACCTGGAGACAGAGTGGCTTGTCTTTCCTGTGGTGGAAAATTGAGCA 4860  
 195 Y Y I G P G D R V A C F A C G G K L S N 214  
 4861 ATTGGGAACCGAAGGATAATGCTATGTGAGAACACCTGAGACATTTTCCCAAATGCCCAT 4920  
 215 W E P K D N A M S E H L R H F P K C P F 234

Fig. 2 (cont.)

4921 TTATAGAAAATCAGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGA 4980  
 235 I E N Q L Q D T S R Y T V S N L S M Q T 254  
 4981 CACATGCAGCCCGCTTTAAACATTCTTTAACTGGCCCTCTAGTGTCTAGTTAATCCTG 5040  
 255 H A A R F K T F F N W P S S V L V N P E 274  
 5041 AGCAGCTTGCAAGTGC GGGTTTTTATTATGTGG<sup>1,2</sup>TAACAGTGATGATGTCAAATGCTTTT 5100  
 275 Q L A S A G F Y Y V G N S D D V K C F C 294  
 5101 GCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCACATGCCA 5160  
 295 C D G G L R C W E S G D D P W V Q H A K 314  
 5161 AGTGGTTTCCAAG<sup>2,3</sup>GTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTCATCCGTCAAG 5220  
 315 W F P R C E Y L I R I K G Q E F I R Q V 334  
 5221 TTCAAGCCAGTTACCCTCATCTACTTGAACAG<sup>3,4</sup>CTGCTATCCACATCAGACAGCCCAGGAG 5280  
 335 Q A S Y P H L L E Q L L S T S D S P G D 354  
 5281 ATGAAAATGCAGAGTCATCA<sup>4,5</sup>TTATCCATTTTGAACCTGGAGAAGACCATTGAGAAGATG 5340  
 355 E N A E S S I I H F E P G E D H S E D A 374  
 5341 CAATCATGATGAATACTCCTGTGATTAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCC 5400  
 375 I M M N T P V I N A A V E M G F S R S L 394  
 5401 TGGTAAAACAGACAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAATTATAGACTAGTCA 5460  
 395 V K Q T V Q R K I L A T G E N Y R L V N 414  
 5461 ATGATCTTGTGTTAGACTTACTCAATGCAGAAGATGAAATAAGGGAAGAGGAGAGAGAAA 5520  
 415 D L V L D L L N A E D E I R E E E R E R 434  
 5521 GAGCAACTGAGGAAAAAGAATCA<sup>5,6</sup>ATGATTTATTATTAATCCGGAAGAATAGAATGGCAC 5580  
 435 A T E E K E S N D L L L I R K N R M A L 454  
 5581 TTTTCAACATTTGACTTGTGTAATCCAATCCTGGATAGTCTACTAACTGCCGGAATTA 5640  
 455 F Q H L T C V I P I L D S L L T A G I I 474  
 5641 TTAATGAACAAGAACATGATGTTATTAAACAGAAGACACAGACGTCTTTACAAGCAAGAG 5700  
 475 N E Q E H D V I K Q K T Q T S L Q A R E 494  
 5701 AACTGATTGATACGATTTTGTAGTAAAGGAAATATTGCAGCCACTGTATTCAGAAACTCTC 5760  
 495 L I D T I L V K G N I A A T V F R N S L 514  
 5761 TGCAAGAAGCTGAAGCTGTGTTATATGAGCATTTATTTG<sup>6,7</sup>TGCAACAGGACATAAAATATA 5820  
 515 Q E A E A V L Y E H L F V Q Q D I K Y I 534  
 5821 TTCCACAGAAGATGTTTCA<sup>7,8</sup>ATCTACAGTGGAAGAACAATTGCGGAGACTACAAGAAG 5880  
 535 P T E D V S D L P V E E Q L R R L Q E E 554  
 5881 AAAGAACATGTAAAGTGTGTATGGACAAAGAAGTGCCATAGTGTATTTCCTTGTGGTC 5940  
 555 R T C K V C M D K E V S I V F I P C G H 574  
 5941 ATCTAGTAGTATGCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCTATTGTAGGAGTA 6000  
 575 L V V C K D C A P S L R K C P I C R S T 594

Fig. 2 (cont.)

6001 CAATCAAGGGTACAGTTCGTACATTTCTTTCATGAAGAAGAACC AAAACATCGTCTAAAC 6060  
595 I K G T V R T F L S \* 604

6061 TTTAGAATTAATTTATTAAATGTATTATAACTTTAACTTTTATCCTAATTTGGTTTCCTT 6120  
6121 AAAATTTTTATTATTACAACTCAAAAAACATTGTTTTGTGTAACATATTATATATGT 6180  
6181 ATCTAAACCATATGAACATATATTTTTTAGAACTAAGAGAATGATAGGCTTTTGTTCCTT 6240  
6241 ATGAACGAAAAAGAGGTAGCACTACAAACACAATATTCAATCAAAATTTTCAGCATTATTG 6300  
6301 AAATTGTAAGTGAAGTAAACTTAAGATATTTGAGTTAACCTTTAAGAATTTTAAATATT 6360  
6361 TTGGCATTGTACTAATACCGGAACATGAAGCCAGGTGTGGTGGTATGTGCCTGTAGTCC 6420  
6421 CAGGCTGAGGCAAGAGAATTACTTGAGCCCAGGAGTTTGAATCCATCCTGGGCAGCATAC 6480  
6481 TGAGACCCTGCCTTTAAAAACAAACAGAACAAAAACAAACACCAGGGACACATTTCTCT 6540  
6541 GTCTTTTTTGATCAGTGCCTATACATCGAAGGTGTGCATATATGTTGAATCACATTTTA 6600  
6601 GGGACATGGTGTTTTATAAAGAATTCTGTGAGAAAAAATTTAATAAAGCAACCAAAAAA 6660  
6661 AAAAAAAA 6669

Fig. 2 (cont.)

T0600T" 25542600

SEQ. ID 7-1 GAGCGCCCGGG<sup>1</sup>~~CT~~<sup>2</sup>GATCCGAGCCGAGCGGGCCGTATCTCCTTGTGCGGCGCCGCTGATTCC 60  
 61 CGGCTCTGCGGAGGCCTCTAGGCAGCCGCGCAGCTTCCGTGTTTGTGCGCCCGCACTGC 120  
 121 ~~G~~<sup>2</sup>~~A~~<sup>3</sup>TTTACAACCCTGAAGAATCTCCCTATCCCTATTTTGTCCCCCTGCAGTAATAAATCCC 180  
 181 ATTATGGAGATCTCGAAACTTTATAAAGGGATATAGTTTGAATTCTATGGAGTGTAATTT 240  
 241 TGTGTATGAATTATATTTTTTAAACATTGAAGAGTTTTTCAGAAAGAAGGCTAGTAGAGTT 300  
 301 GATTACTGATACTTTATGCTAAGCAGTACTTTTTTGGTAGTACAATATTTTGTAGGCGT 360  
 361 TTCTGATAACACTAGAAAGGACAAGTTTTATCTTGTGATAAATTGATTAATGTTTACAAC 420  
 421 ATGACTGATAATTATAGCTGAATAGTCCTTAAATGATGAACAGGTTATTTAGTTTTTAAA 480  
 481 TGCAGTGTA AAAAGTGTGCTGTGGAAATTTTATGGCTAACTAAGTTTATGGAGAAAATAC 540  
 541 CTTCA GTTGATCAAGAATAATAGTGGTATACAAAGTTAGGAAGAAAGTCAACATGATGCT 600  
 601 GCAGGAAATGGAAACAAATACAAATGATATTTAACAAGATAGAGTTTACAGTTTTTGAA 660  
 661 CTTTAAGCCAAATTCATTTGACATCAAGCACTATAGCAGGCACAGGTTCAACAAAGCTTG 720  
 721 TGGGTATTGACTTCCCCCAAAGTTGTGAGCTGAAGTAATTTAGCCCACTTAAGTAAATA 780  
 781 CTATGATGATAAGCTGTGTGAACCTAGCTTTTAAATAGTGTGACCATATGAAGGTTTTAA 840  
 841 TTACTTTTGTTTATTGGAATAAAATGAGATTTTTTGGGTTGTCATGTTAAAGTGCTTATA 900  
 901 GGGAAAGAAGCCTGCATATAATTTTTTACCTTGTGGCATAATCAGTAATTGGTCTGTTAT 960  
 961 TCAGGCTTCATAGCTTGTAAACARATATAAATAAAAGGCATAATTTAGGTATTCTATAGT 1020  
 1021 TGCTTAGAATTTTGTTAATATAAATCTCTGTGAAAAATCAAGGAGTTTAAATATTTTCAG 1080  
 1081 AAGTGCATCCACCTTTTCAGGGCTTAAAGTTAGTATTAACCAAGATTATGAACAAATAGC 1140  
 1141 ACTTAGGTTACCTGAAAGAGTTACTACAACCCCAAAGAGTTGTGTTCTAAGTAGTATCTT 1200  
 1201 GGTAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAATCCAGTAAAGAA 1260  
 1261 AGTGTAGTAAATTCTACATAAGAGTCTATCATTGATTTCTTTTTGTGGTAAAAATCTTAG 1320  
 1321 TTCATGTGAAGAAATTTTCATGTGAATGTTTTAGCTATCAAACAGTACTGTACCTACTCA 1380  
 1381 TGCACAAAACCTGCCTCCCAAAGACTTTTCCAGGTCCCTCGTATCAAACATTAAAGAGTA<sup>M</sup> 1440  
 SEQ. ID 8-2 H K T A S Q R L F P G P S Y Q N I K S I 21  
 1441 TAATGGAAGATAGCAGGATCTTGTGAGATTGGACAAACAGCAACAAACAAAAATGAAGT 1500  
 22 M E D S T I L S D W T N S N K Q K M K Y 41  
 1501 ATGACTTTTCTGTGAACCTCTACAGAATGTCTACATATTCAACTTTCCCGCCGGGGTGC 1560  
 42 D F S C E L Y R M S T Y S T F P A G V P 61  
 1561 CTGTCTCAGAAAGGAGTCTTGCTCGTGTGTTTATTATACTGGTGTGAATGACAAGG 1620  
 62 V S E R S L A R A G F Y Y T G V N D K V 81  
 1621 TCAAATGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAACTAGGAGACAGTCTTATTC 1680  
 82 K C F C C G L M L D N W K L G D S P I Q 101  
 1681 AAAAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTCAGAATCTGGTTTCAGCTAGTC 1740  
 102 K H K Q L Y P S C S F I Q N L V S A S L 121  
 1741 TGGGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTTGCACATTCATTATCTC 1800  
 122 G S T S K N T S P M R N S F A H S L S P 141  
 1801 CCACCTTGGAACATAGTAGCTTGTTCAGTGGTTCTTACTCCAGCCTTCTCCAAACCCCTC 1860  
 142 T L E H S S L F S G S Y S S L S P N P L 161  
 1861 TTAATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCTACAGTTATGCAA 1920  
 162 N S R A V E D I S S S R T N P Y S Y A M 181  
 1921 TGAGTACTGAAGAAGCCAGATTTCTTACCTACCATATGTGGCCATTAACTTTTTTGTAC 1980  
 182 S T E E A R F L T Y H M W P L T F L S P 201

Fig. 3



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1981 CATCAGAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGGTAGCCTGCT 2040  
 202 S E L A R A G F Y Y I G P G D R V A C F 221

2041 TTGCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAAGGATGATGCTATGTCAGAACACC 2100  
 222 A C G G K L S N W E P K D D A M S E H R 241

2101 GGAGGCATTTTCCCAACTGTCCATTTTGGAAAATTCTCTAGAACTCTGAGGTTTAGCA 2160  
 242 R H F P N C P F L E N S L E T L R F S I 261

2161 TTTCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTTATGTACTGGCCAT 2220  
 262 S N L S M Q T H A A R M R T F M Y W P S 281

2221 CTAGTGTTCCAGTTCAGCCTGAGCAGCTTGCAAGTGTGGTTTTTATTATGTGGTTCGCA 2280  
 282 S V P V Q P E Q L A S A G F Y Y V G R N 301

2281 ATGATGATGTCAAATGCTTTTGTGTGATGGTGGCTTGAGGTGTTGGGAATCTGGAGATG 2340  
 302 D D V K C F C C D G G L R C W E S G D D 321

2341 ATCCATGGGTAGAACATGCCAAGTGGTTTCCAAGTGTGAGTTCTTGATACGAATGAAAG 2400  
 322 P W V E H A K W F P R C E F L I R M K G 341

2401 GCCAAGAGTTTGTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGTGTGT 2460  
 342 Q E F V D E I Q G R Y P H L L E Q L L S 361

2461 CAACTTCAGATACCACTGGAGAAGAAAATGCTGACCCACCAATTATTCATTTTGGACCTG 2520  
 362 T S D T T G E E N A D P P I I H F G P G 381

2521 GAGAAAGTTCTTCAGAAGATGCTGTGATGATGAATACACCTGTGGTTAAATCTGCCTTGG 2580  
 382 E S S S E D A V M M N T P V V K S A L E 401

2581 AAATGGGCTTTAATAGAGACCTGGTGAAACAAACAGTTCAAAGTAAATCCTGACAACTG 2640  
 402 M G F N R D L V K Q T V Q S K I L T T G 421

2641 GAGAGAACTATAAAACAGTTAATGATATTGTGTCAGCACTTCTTAATGCTGAAGATGAAA 2700  
 422 E N Y K T V N D I V S A L L N A E D E K 441

2701 AAAGAGAAGAGGAGAAGGAAAAACAAGCTGAAGAAATGGCATCAGATGATTGTGATTAA 2760  
 442 R E E E K E K Q A E E M A S D D L S L I 461

2761 TTCGAAGAACAGAATGGCTCTCTTCAACAATTGACATGTGTGCTTCCTATCCTGGATA 2820  
 462 R K N R M A L F Q Q L T C V L P I L D N 481

2821 ATCTTTTAAAGGCCAATGTAATTAATAAACAGGAACATGATATTATTAAACAAAAACAC 2880  
 482 L L K A N V I N K Q E H D I I K Q K T Q 501

2881 AGATACCTTTACAAGCGAGAGAACTGATTGATACCATTTTGGTTAAAGGAAATGCTGCGG 2940  
 502 I P L Q A R E L I D T I L V K G N A A A 521

2941 CCAACATCTTCAAAAAGTGTCTAAAAGAAATTGACTCTACATTGTATAAGAACTTATTTG 3000  
 522 N I F K N C L K E I D S T L Y K N L F V 541

3001 TGGATAAGAATATGAAGTATATCCCAACAGAAGATGTTTCAGTCTGTCACTGGAAGAAC 3060  
 542 D K N M K Y I P T E D V S G L S L E E Q 561

Fig. 3 (cont.)

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3061 AATTGAGGAGGTTGCAAGAAGAACGAACCTGTAAAGTGTGTATGGACAAAGAAGTTTCTG 3120  
562 L R R L Q E E R T C K V C M D K E V S V 581

3121 TTGTATTTATTCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTGCCCTTCTCTAAGAA 3180  
582 V F I P C G H L V V C Q E C A P S L R K 601

3181 AATGCCCTATTTGCAGGGGTATAATCAAGGGTACTGTTTCGTACATTTCTCTCTTAAAGAA 3240  
602 C P I C R G I I K G T V R T F L S \* 618

3241 AAATAGTCTATATTTTAACCTGCATAAAAAGGTCTTTAAATATTGTTGAACACTTGAAG 3300  
3301 CCATCTAAAGTAAAAAGGAATTATGAGTTTTTCAATTAGTAACATTCATGTTCTAGTCT 3360  
3361 GCTTTGGTACTAATAATCTTGTCTGAAAAGATGGTATCATATATTTAATCTTAATCTG 3420  
3421 TTTATTTACAAGGGAAGATTATGTTTGGTGAACATATATTAGTATGTATGTGTACCTAAG 3480  
3481 GGAGTAGTGTCACTGCTTGTATGCATCATTTTCAGGAGTTACTGGATTTGTTGTTCTTTC 3540  
3541 AGAAAGCTTTGAATACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACCTGGAG 3600  
3601 TTCATCAGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTGTTTTAAATAAG 3660  
3661 GATTTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAA 3720  
3721 AGAAAAAAAAA 3732

Fig. 3 (cont.)

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SEQ. ID 9-1 ATTTTAAATTGATGCATTAACATTCTAAACATTCTGTTTTTAAATAGTAAAAATT 60  
 61 GAACTTGCCTTGAATATGTAATGATTCATTATAACAATTATGCATAGTCTTTAATAATC 120  
 121 TGCATATTTTATGCTGCTTTTCATGTTTTTCCTAATTAATGACTTCACATGTTAATATTT 180  
 181 ATAATTTTCTGTCATAGTTTCCATATTTATATAAAATGAATACTTAAGATCAGTAATTC 240  
 241 TGCTCTGTTTGTATATACTATTTTCCATCAAAAGACAAAATGGGACTGAGGTTGAGGC 300  
 301 TCGTTGCTAAAGCACTTTCCTAAAATGCAAAAGGCCCTATGATGGATCCCTAGTACTTAT 360  
 361 TTAAGTGAGAGAGAAACAGGCTGGGGGTGTAGGTCTGTTAGAGCATGTGTTTGGCATTAT 420  
 421 GTGAAGCCCAACACTAAAAAAGGAGAACAACAAGCGCAGACTTTAAACTCAAGTG 480  
 481 GTTTGGTAATGTACGACTCTACTGTTTAGAATTAATAATGTGTCTTAGTTATTGTGCCATT 540  
 541 ATTTTATGTCATCACTGATAATATATTAGTGCTTAGTATCAGAAATAGTCCTTATGCT 600  
 601 TTGTGTTTTGAAGTTCCTAATGCAATGTTCTCTTTCTAGAAAAGGTGGACAAGTCTTATT 660  
 661 TTCCAGAGAAGATGACTTTTAACAGTTTGAAGGAAGTGAAGTCTTTGTACTTGCAGACA 720  
 SEQ. ID 10-1 M T F N S F E G T R T F V L A D T 17  
 721 CCAATAAGGATGAAGAATTTGTAGAAGAGTTTAATAGATTAAAAACATTTGCTAATCTCC 780  
 18 N K D E E F V E E F N R L K T F A N F P 37  
 781 CAAGTAGTAGTCCTGTTTCAGCATCAACATTGGCGGAGCTGGGTTTCTTTATACCGGTG 840  
 38 S S S P V S A S T L A R A G F L Y T G E 57  
 841 AAGGAGACACCGTGCAATGTTTCAGTTGTCATGCGGCAATAGATAGATGGCAGTATGGAG 900  
 58 G D T V Q C F S C H A A I D R W Q Y G D 77  
 901 ACTCAGCTGTTGGAAGACACAGGAGAATATCCCCAAATTGCAGATTTATCAATGGTTTTT 960  
 78 S A V G R H R R I S P N C R F I N G F Y 97  
 961 ATTTTGAAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAAAT 1020  
 98 F E N G A A Q S T N P G I Q N G Q Y K S 117  
 1021 CTGAAAACGTGTGGGAAATAGAAATCCTTTTGCCCTGACAGGCCACCTGAGACTCATG 1080  
 118 E N C V G N R N P F A P D R P P E T H A 137  
 1081 CTGATTATCTCTTGAGAACTGGACAGGTTGTAGATATTTAGACACCATATACCCGAGGA 1140  
 138 D Y L L R T G Q V V D I S D T I Y P R N 157  
 1141 ACCCTGCCATGTGTAGTGAAGAAGCCAGATTGAAGTCATTTAGAACTGGCCGGACTATG 1200  
 158 P A M C S E E A R L K S F Q N W P D Y A 177  
 1201 CTCATTTAACCCCCAGAGAGTTAGCTAGTGCTGGCCTCTACTACACAGGGGCTGATGATC 1260  
 178 H L T P R E L A S A G L Y Y T G A D D Q 197  
 1261 AAGTGCAATGCTTTTGTGTGGGGGAAAACGTGAAAATGGGAACCTGTGATCGTGCTT 1320  
 198 V Q C F C C G G K L K N W E P C D R A W 217  
 1321 GGTGAGAACACAGGAGACACTTTCCCAATTGCTTTTTTGTGTTTGGGCCGGAACGTTAATG 1380  
 218 S E H R R H F P N C F F V L G R N V N V 237  
 1381 TTCGAAGTGAATCTGGTGTGAGTTCTGATAGGAATTTCCCAAATTCACAACTCTCCAA 1440  
 238 R S E S G V S S D R N F P N S T N S P R 257  
 1441 GAAATCCAGCCATGGCAGAATATGAAGCACGGATCGTTACTTTTGAACATGGACATCCT 1500  
 258 N P A M A E Y E A R I V T F G T W T S S 277

Fig. 4

FIGURE 4

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1501 CAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAG 1560  
278 V N K E Q L A R A G F Y A L G E G D K V 297

1561 TGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGG 1620  
298 K C F H C G G G L T D W K P S E D P W D 317

1621 ACCAGCATGCTAAGTGCTACCCAGGGTGTCAAATACCTATTGGATGAGAAGGGGCAAGAAT 1680  
318 Q H A K C Y P G C K Y L L D E K G Q E Y 337

1681 ATATAAATAATATTCATTTAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAA 1740  
338 I N N I H L T H P L E E S L G R T A E K 357

1741 AAACACCACCGCTAACTAAAAAATCGATGATACCATCTTCCAGAATCCTATGGTGCAAG 1800  
358 T P P L T K K I D D T I F Q N P M V Q E 377

1801 AAGCTATACGAATGGGATTTAGCTTCAAGGACCTTAAGAAAACAATGGAAGAAAAAATCC 1860  
378 A I R M G F S F K D L K K T M E E K I Q 397

1861 AAACATCCGGGAGCAGCTATCTATCACTTGAGGTCCTGATTGCAGATCTTGTGAGTGCTC 1920  
398 T S G S S Y L S L E V L I A D L V S A Q 417

1921 AGAAAGATAATACGGAGGATGAGTCAAGTCAAACCTTCATTGCAGAAAGACATTAGTACTG 1980  
418 K D N T E D E S S Q T S L Q K D I S T E 437

1981 AAGAGCAGCTAAGGCGCCTACAAGAGGAGAAGCTTTCCAAAATCTGTATGGATAGAAATA 2040  
438 E Q L R R L Q E E K L S K I C M D R N I 457

2041 TTGCTATCGTTTTTTTTTCTTGTGGACATCTGGCCACTTGTAACAGTGTGCAGAAGCAG 2100  
458 A I V F F P C G H L A T C K Q C A E A V 477

2101 TTGACAAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAAAATTTTTATGTCTT 2160  
478 D K C P M C Y T V I T F N Q K I F M S \* 496

2161 AGTGGGGCACCACATGTTATGTTCTTCTTGCTCTAATTGAATGTGTAATGGGAGCGAACT 2220  
2221 TTAAGTAATCCTGCATTTGCATTCCATTAGCATCCTGCTGTTTCCAAATGGAGACCAATG 2280  
2281 CTAACAGCACTGTTTCCGTCTAAACATTCAATTTCTGGATCTTTTCGAGTTATCAGCTGTA 2340  
2341 TCATTTAGCCAGTGTCTTACTCGATTGAAACCTTAGACAGAGAAGCATTTTATAGCTTTT 2400  
2401 CACATGTATATTGGTAGTACACTGACTTGATTTCTATATGTAAGTGAATTCATCACCTGC 2460  
2461 ATGTTTCATGCCTTTTGCATAAGCTTAACAAATGGAGTGTCTGTATAAGCATGGAGATG 2520  
2521 TGATGGAATCTGCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAAGAACTGCCCCA 2580  
2581 CGCTGCTGGGAGGATAAAGATTGTTTTAGATGCTCACTTCTGTGTTTTAGGATTCTGCCC 2640  
2641 ATTTACTTGAATTTATTGGAGTTATAATGTACTTATATGATATTCCGAA 2691

Fig. 4 (cont.)

1. **What is the purpose of the document?**  
 2. **What are the main findings of the study?**  
 3. **What are the implications of the findings?**  
 4. **What are the limitations of the study?**  
 5. **What are the conclusions of the study?**

**Fig. 5**

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1261 TGCTCAGAATCAAAGGCCAAGAATTTGTCTAGCCAAAGTTCAAGCTGGCTATCCTCATCTAC 1320  
 321 L R I K G Q E F V S Q V Q A G Y P H L L 340  
 1321 TTGAGCAGCTATTATCTACGTCAGACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCG 1380  
 341 E Q L L S T S D S P E D E N A D A A I V 360  
 1381 TGCATTTTGGCCCTGGAGAAAGTTCGGAAGATGTCGTCATGATGAGCACGCCTGTGGTTA 1440  
 361 H F G P G E S S E D V V M M S T P V V K 380  
 1441 AAGCAGCCTTGAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGCGGCAGA 1500  
 381 A A L E M G F S R S L V R Q T V Q R Q I 400  
 1501 TCCTGGCCACTGGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATG 1560  
 401 L A T G E N Y R T V S D L V I G L L D A 420  
 1561 CAGAAGACGAGATGAGAGAGGAGCAGATGGAGCAGGCGGCCGAGGAGGAGGAGTCAGATG 1620  
 421 E D E M R E E Q M E Q A A E E E E S D D 440  
 1621 ATCTAGCACTAATCCGGAAGAACAAAATGGTGCTTTTCCAACATTTGACGTGTGTGACAC 1680  
 441 L A L I R K N K M V L F Q H L T C V T P 460  
 1681 CAATGCTGTATTGCCTCCTAAGTGCAAGGGCCATCACTGAACAGGAGTGCAATGCTGTGA 1740  
 461 M L Y C L L S A R A I T E Q E C N A V K 480  
 1741 AACAGAAACCACACACCTTACAAGCAAGCACACTGATTGATACTGTGTTAGCAAAAGGAA 1800  
 481 Q K P H T L Q A S T L I D T V L A K G N 500  
 1801 ACACTGCAGCAACCTCATTGAGAACTCCCTTCGGGAAATTGACCCTGCGTTATACAGAG 1860  
 501 T A A T S F R N S L R E I D P A L Y R D 520  
 1861 ATATATTTGTGCAACAGGACATTAGGAGTCTTCCACAGATGACATTGCAGCTCTACCAA 1920  
 521 I F V Q Q D I R S L P T D D I A A L P M 540  
 1921 TGGAAGAACAGTTGCGGAACTCCAGGAGGAAAGAATGTGTAAAGTGTGTATGGACCGAG 1980  
 541 E E Q L R K L Q E E R M C K V C M D R E 560  
 1981 AGGTATCCATCGTGTTCATTCCCTGTGGCCATCTGGTCGTGTGCAAAGACTGCGCTCCCT 2040  
 561 V S I V F I P C G H L V V C K D C A P S 580  
 2041 CTCTGAGGAAGTGTCCTATCTGTAGAGGGACCATCAAGGGCAGAGTGGCGACATTTCTCT 2100  
 581 L R K C P I C R G T I K G T V R T F L S 600  
 2101 CCTGAACAAGACTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACTGTCACT 2160  
 \*  
 2161 CCCAGCTCCATTTCGGAAGTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACACACA 2220  
 2221 AATATAAACATGAAAACTTTTGTCTGAAGTCAAGAATGAATGAATTACTTATATAATAA 2280  
 2281 TTTTAATTGGTTTCTTAAAGTGCTATTTGTTCCCAACTCAGAAAATTGTTTCTGTAA 2340  
 2341 ACATATTTACATACTACCTGCATCTAAAGTATTCATATATTCATATATTCAGATGTCATG 2400  
 2401 AGAGAGGGTTTTGTTCTTGTTCCTGAAAAGCAGGGATTGCCTGCACTCCTGAAATTCTCA 2460  
 2461 GAAAGATTTACAATGTTGGCATTATGGTTTCAGAACTAGAATCTTCCCGTTGCTTTA 2520  
 2521 AGAACCGGGAGCACAGATGTCCATGTGTTTTATGTATAGAAATTCCTGTTATTTATTGGA 2580  
 2581 TGACATTTTAGGGATATGAAATTTTATAAAGAATTTGTGAGAAAAAGTTAATAAGCAA 2640  
 2641 CATAATTACCTCTTTTTTTTTTAAAGAAAAA 2676

Fig. 5 (cont.)

SEQ. ID 13-1 AGTTATATAAAATACGAAGTTTTCAAAAAGAAGGCTAGTGCAACAGAAAAGCTTTGCTAA 60  
 61 AACAGATTCTTAGTTATTTGAGGTAACAAAAGAAAGCCATGTCTTGAATTGATTGCTTCT 120  
 121 TAATTATAACAGACTTATAGTGGAAGGGCCTTAAACACAGGCGGACTTTATAAAATGCA 180  
 181 GTCTTAGGTTTATGTGCAAAATACTGTCTGTTGACCAGATGTATTACATGATATATACA 240  
 241 GAGTCAAGGTGGTGATATAGAAGATTTAACAGTGAGGGAGTTAACAGTCTGTGCTTTAAG 300  
 301 CGCAGTTCCTTTACAGTGAATACTGTAGTCTTAATAGACCTGAGCTGACTGCTGCAGTTG 360  
 361 ATGTAACCCACTTTAGAGAATACTGTATGACATCTTCTCTAAGGAAAACCAGCTGCAGAC 420  
 421 TTCACTCAGTTCCTTTTCAATTCATAGGAAAAGGAGTAGTTTCAGATGTCATGTTTAAGTCC 480  
 481 TTATAAGGGAAAAGAGCCTGAATATATGCCCTAGTACCTAGGCTTCATAACTAGTAATAA 540  
 541 GAAGTTAGTTATGGGTAAATAGATCTCAGGTTACCCAGAAGAGTTTCATGTGACCCCCAAA 600  
 601 GAGTCCTAACTAGTGTCTTGGCAAGTGAGACAGATTTGTCTGTGAGGGTGTCAATTCAC 660  
 661 CAGTCCAAGCAGAAGACAATGAATCTATCCAGTCAGGTGTCTGTGGTGGAGATCTAGTGT 720  
 721 CCAAGTGGTGAGAACTTCATCTGGAAGTTTAAGCGGTCAGAAATACTATTACTACTCAT 780  
 1 M 1

781 GGACAAAACGTCTCTCCAGAGACTCGGCCAAGGTACCTTACACCAAAAACCTTAAACGTAT 840  
 SEQ. ID 14-2 D K T V S Q R L G Q G T L H Q K L K R I 21

841 AATGGAGAAGAGCACAATCTTGTCAAATTGGACAAAGGAGAGCGAAGAAAAATGAAGTT 900  
 22 M E K S T I L S N W T K E S E E K M K F 41

901 TGACTTTTCGTGTGAACCTCTACCGAATGTCTACATATTCAGCTTTTCCAGGGGAGTTCC 960  
 42 D F S C E L Y R M S T Y S A F P R G V P 61

961 TGTCTCAGAGAGGAGTCTGGCTCGTGCTGGCTTTTATTATACAGGTGTGAATGACAAAGT 1020  
 62 V S E R S L A R A G F Y Y T G V N D K V 81

1021 CAAGTGCTTCTGCTGTGGCCTGATGTTGGATAACTGGAACAAGGGGACAGTCTCTGTTGA 1080  
 82 K C F C C G L M L D N W K Q G D S P V E 101

1081 AAAGCACAGACAGTTCTATCCCAGCTGCAGCTTTGTACAGACTCTGCTTTTCAGCCAGTCT 1140  
 102 K H R Q F Y P S C S F V Q T L L S A S L 121

1141 GCAGTCTCCATCTAAGAATATGTCTCCTGTGAAAAGTAGATTTGCACATTCGTCACCTCT 1200  
 122 Q S P S K N M S P V K S R F A H S S P L 141

1201 GGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCCTCTTAATTCTAGAGCAGTGGA 1260  
 142 E R G G I H S N L C S S P L N S R A V E 161

1261 AGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCATGAGTACAGAAGAGGCCAGATT 1320  
 162 D F S S R M D P C S Y A M S T E E A R F 181

1321 TCTTACTTACAGTATGTGGCCTTTAAGTTTTCTGTCAACAGCAGAGCTGGCCAGAGCTGG 1380  
 182 L T Y S M W P L S F L S P A E L A R A G 201

1381 CTTCTATTACATAGGGCCTGGAGACAGGGTGGCCTGTTTTGCCTGTGGTGGGAAACTGAG 1440  
 202 F Y Y I G P G D R V A C F A C G G K L S 221

1441 CAACTGGGAACCAAAGGATGATGCTATGTCAGAGCACCGCAGACATTTTCCCCACTGTCC 1500  
 222 N W E P K D D A M S E H R R H F P H C P 241

1501 ATTTCTGGAAAATACTTCAGAAACACAGAGGTTTAGTATATCAAATCTAAGTATGCAGAC 1560  
 242 F L E N T S E T Q R F S I S N L S M Q T 261

Fig. 6

1561 ACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACCTAGTGTTCTGTTTCAGCCCCGA 1620  
 262 H S A R L R T F L Y W P P S V P V Q P E 281  
 1621 GCAGCTTGCAAGTCTGGATTCTATTACGTGGATCGCAATGATGATGTCAAGTGCTTTTG 1680  
 282 Q L A S A G F Y Y V D R N D D V K C F C 301  
 1681 TTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGACCCCTGGATAGAACACGCCAA 1740  
 302 C D G G L R C W E P G D D P W I E H A K 321  
 1741 ATGGTTTCCAAG<sup>1</sup>GTGTGAGTTCTTGATACGGATGAAGGGTCAGGAGTTTGTGATGAGAT 1800  
 322 W F P R C E F L I R M K G Q E F V D E I 341  
 1801 TCAAGCTAGATATCCTCATCTTCTTGAGCAG<sup>2</sup>CTGTTGTCCACTTCAGACACCCCAGGAGA 1860  
 342 Q A R Y P H L L E Q L L S T S D T P G E 361  
 1861 AGAAATGCTGACCCCTACAGAGACAGTGGTGCATTTTGGCCCTGGAGAAAGTTCGAAAGA 1920  
 362 E N A D P T E T V V H F G P G E S S K D 381  
 1921 TGTCGTCATGATGAGCACGCCTGTGGTTAAAGCAGCCTTGGAATGGGCTTCAGTAGGAG 1980  
 382 V V M M S T P V V K A A L E M G F S R S 401  
 1981 CCTGGTGAGACAGACGGTTCAGCGGCAGATCCTGGCCACTGGTGAGAACTACAGGACCGT 2040  
 402 L V R Q T V Q R Q I L A T G E N Y R T V 421  
 2041 CAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGAGAGAAGAGAAGAGGAGAAGGA 2100  
 422 N D I V S V L L N A E D E R R E E E K E 441  
 2101 AAGACAGACTGAAGAGATGGCATCAG<sup>4</sup>GTGACTTATCACTGATTCCGAAGAATAGAATGGC 2160  
 442 R Q T E E M A S G D L S L I R K N R M A 461  
 2161 CCTCTTTCAACAGTTGACACATGTCCTTCCTATCCTGGATAATCTTCTTGAGGCCAGTGT 2220  
 462 L F Q Q L T H V L P I L D N L L E A S V 481  
 2221 AATTACAAAACAGGAACATGATATTATTAGACAGAAAACACAGATACCCCTTACAAGCAAG 2280  
 482 I T K Q E H D I I R Q K T Q I P L Q A R 501  
 2281 AGAGCTTATTGACACCGTTTTAGTCAAGGGAAATGCTGCAGCCAACATCTTCAAAAACCTC 2340  
 502 E L I D T V L V K G N A A A N I F K N S 521  
 2341 TCTGAAGGAAATTGACTCCACGTTATATGAAAACCTTATTTG<sup>5</sup>TGGAAAAGAATATGAAGTA 2400  
 522 L K E I D S T L Y E N L F V E K N M K Y 541  
 2401 TATTC AACAGAAGACGTTTCA<sup>6</sup>GGCTTGTCATTGGAAGAGCAGTTGCGGAGATTACAAGA 2460  
 542 I P T E D V S G L S L E E Q L R R L Q E 561  
 2461 AGAACGAACTTGCAAAGTGTGTATGGACAGAGAGGTTTCTATTGTGTTTATTCCGTGTGG 2520  
 562 E R T C K V C M D R E V S I V F I P C G 581  
 2521 TCATCTAGTAGTCTGCCAGGAATGTGCCCCCTTCTCTAAGGAAGTGCCCCATCTGCAGGGG 2580  
 582 H L V V C Q E C A P S L R K C P I C R G 601  
 2581 GACAATCAAGGGGACTGTGCGCACATTTCTCTCATGAGTGAAGAATGGTCTGAAAGTATT 2640  
 602 T I K G T V R T F L S \* 612

Fig. 6 (cont.)



2641 GTTGGACATCAGAAGCTGTCAGAACAAAGAATGAACTACTGATTTTCAGCTCTTCAGCAGG 2700  
2701 ACATTCTACTCTCTTTCAAGATTAGTAATCTTGCTTTATGAAGGGTAGCATTGTATATTT 2760  
2761 AAGCTTAGTCTGTTGCAAGGGAAGGTCTATGCTGTTGAGCTACAGGACTGTGTCTGTTCC 2820  
2821 AGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGACTTCTTGGATTGGAATTTGT 2880  
2881 GAAAGCTTTGGATTTCAGGTGATGTGGAGCTCAGAAATCCTGAAACCAGTGGCTCTGGTAC 2940  
2941 TCAGTAGTTAGGGTACCCTGTGCTTCTTGCTGCTTTTCTTTCTGGAAAATAAGGATTTT 3000  
3001 TCTGCTACTGGTAAATATTTTCTGTTTGTGAGAAATATATTAAAGTGTTCCTTTTAAAGG 3060  
3061 CGTGCATCATTGTAGTGTGTGCAGGGATGTATGCAGGCAAAACACTGTGTATATAATAAA 3120  
3121 TAAATCTTTTTTAAAAAGTGTAACAAAAA 3151

Fig. 6 (cont.)

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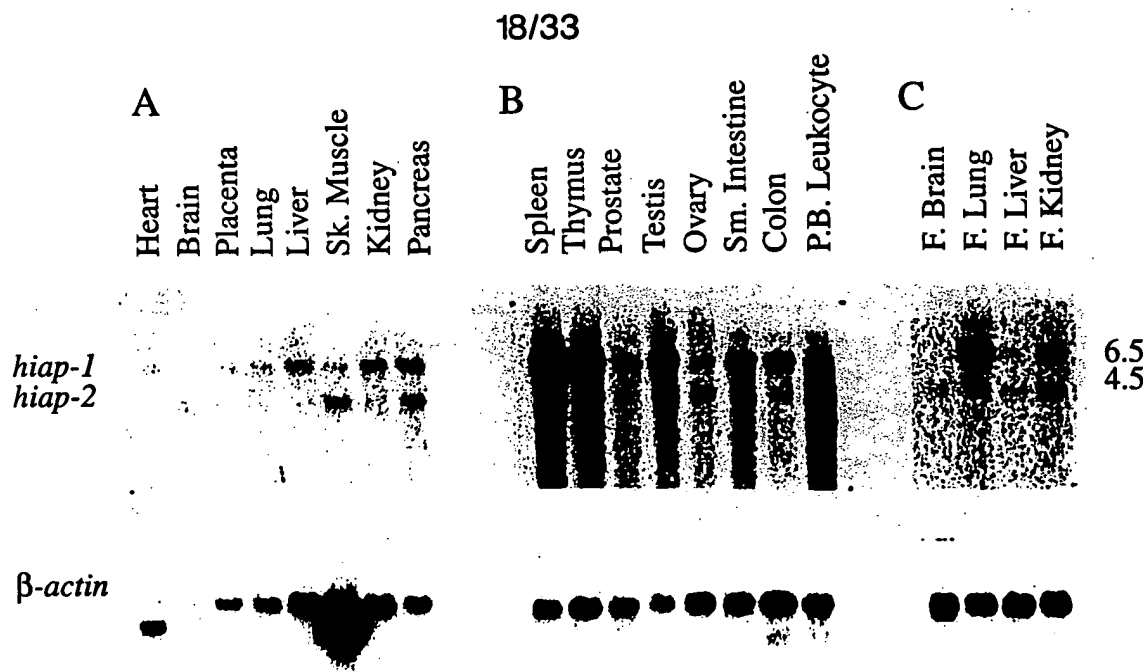


Fig. 7

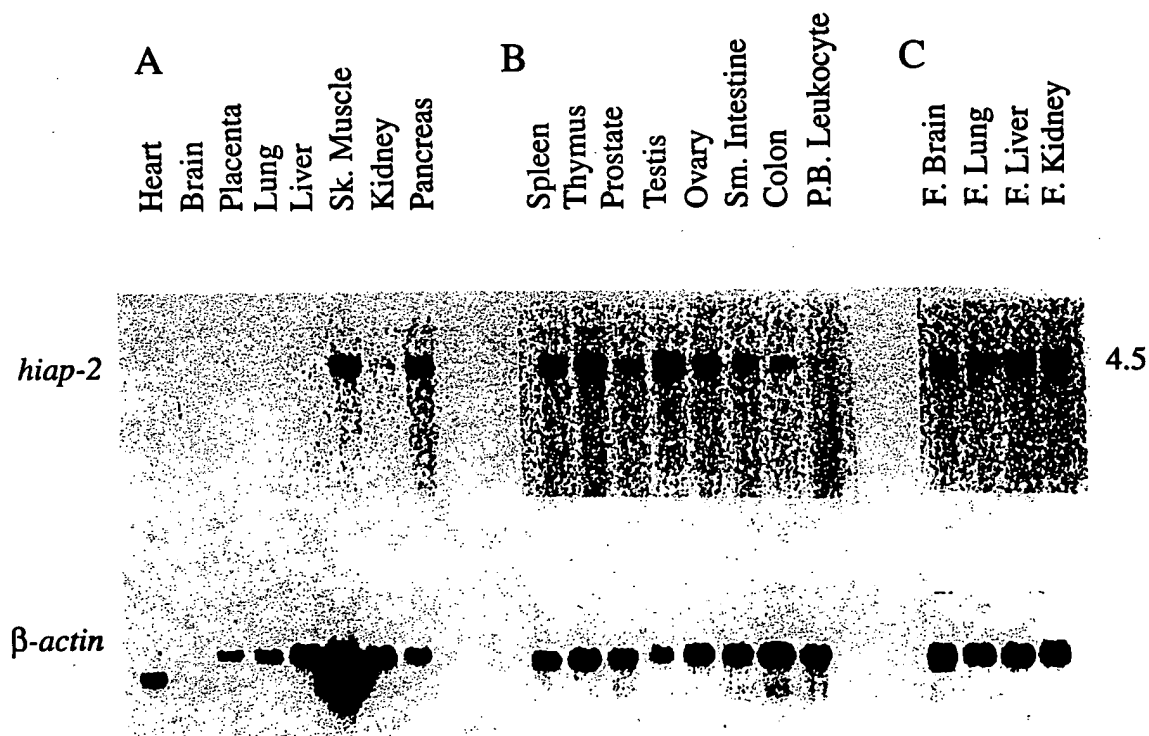


Fig. 8

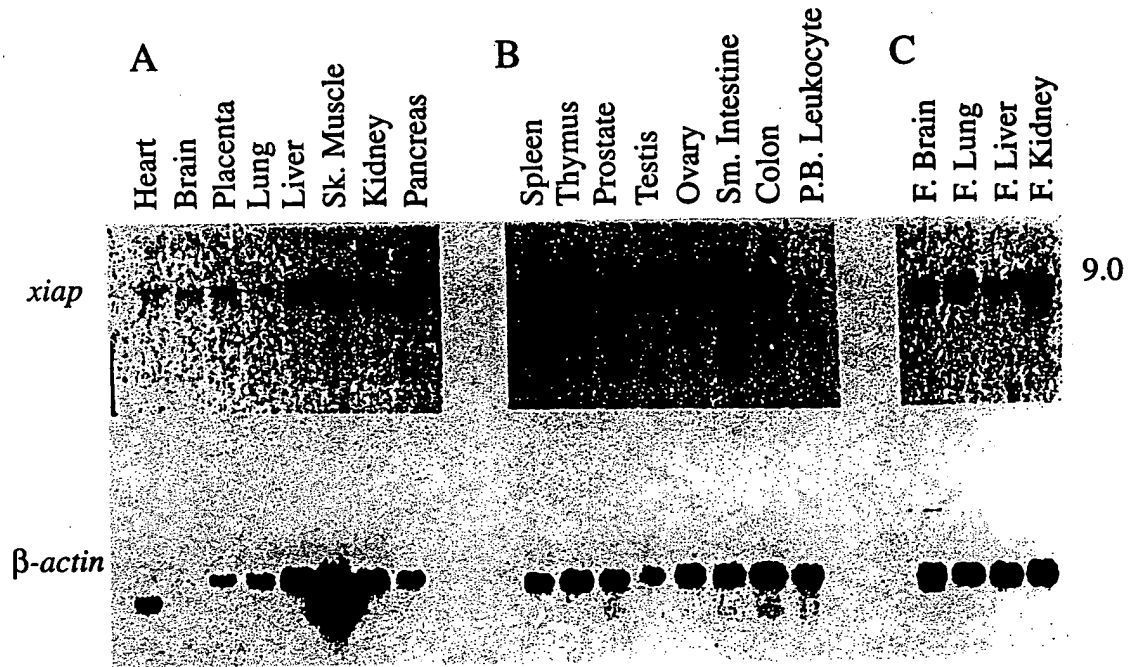


Fig. 9

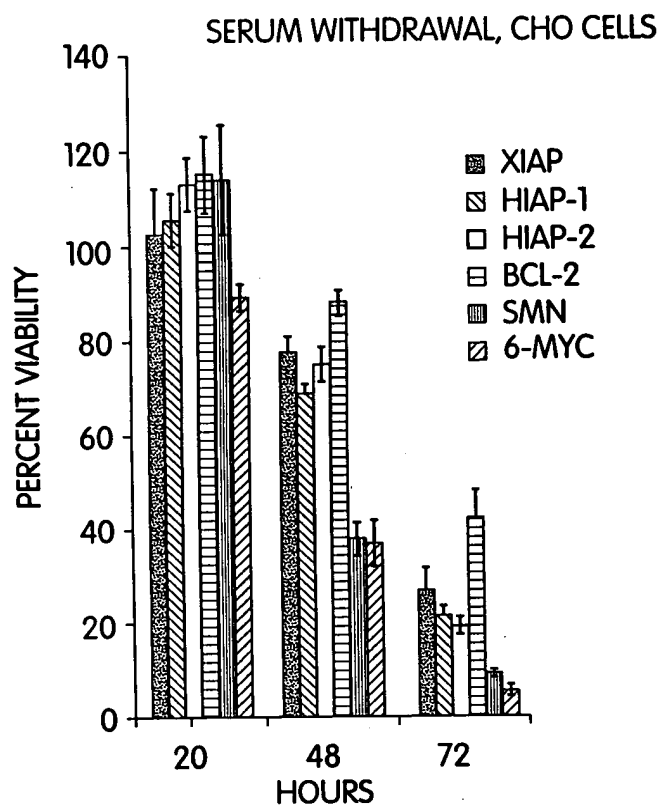


Fig. 10A

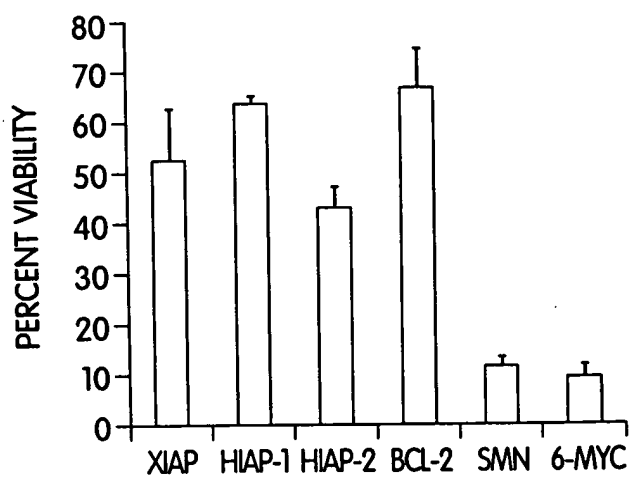
MENADIONE (20 $\mu$ M), CHO CELLS. 24hr SURVIVAL

Fig. 10B

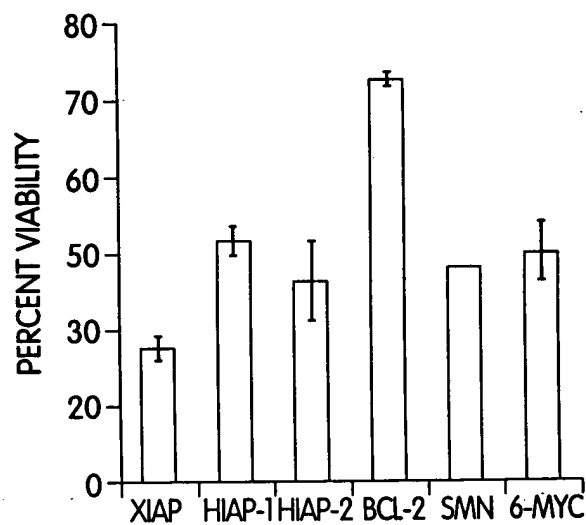
STAUROSPOURINE ( $1\mu\text{M}$ ), RAT-1 CELLS, 24 HOUR SURVIVAL

Fig. 10C

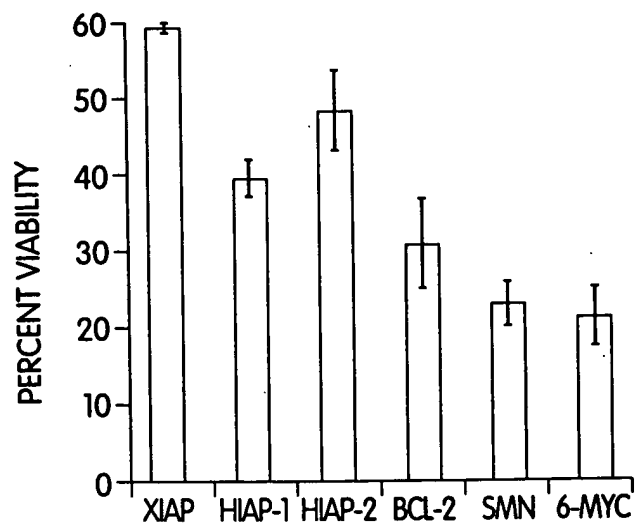
MENADIONE ( $10\mu\text{M}$ ), RAT-1 CELLS, 18 HOUR SURVIVAL

Fig. 10D

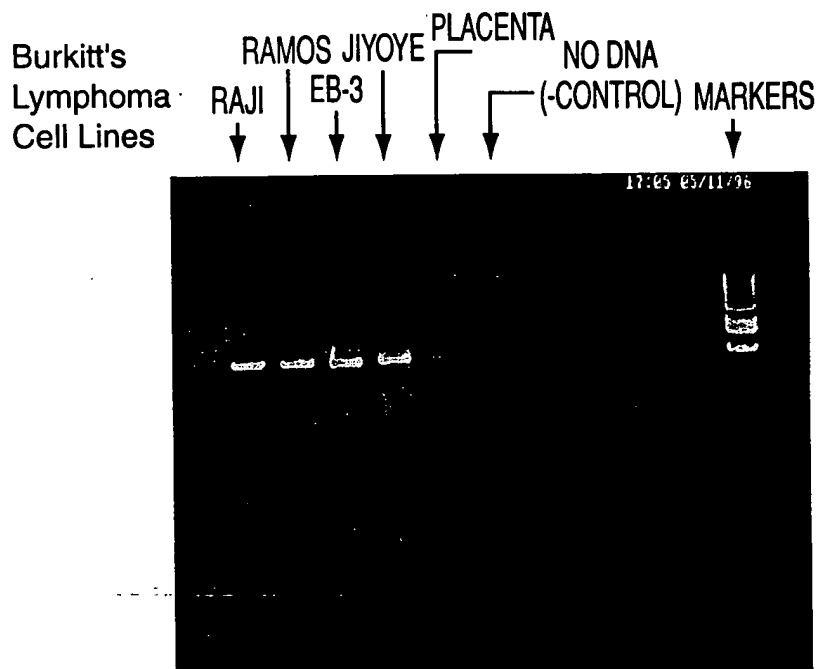


Fig. 11

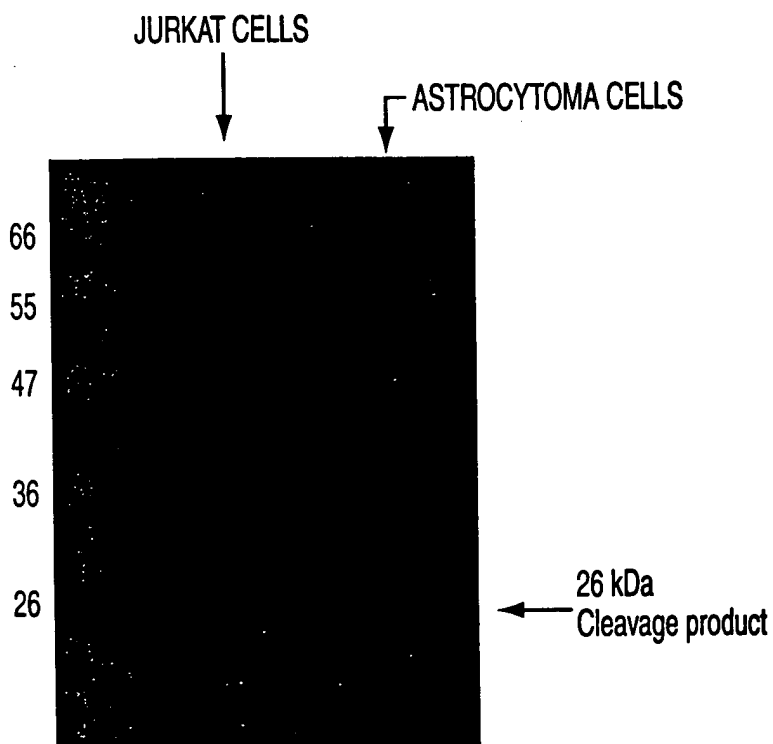


Fig. 12

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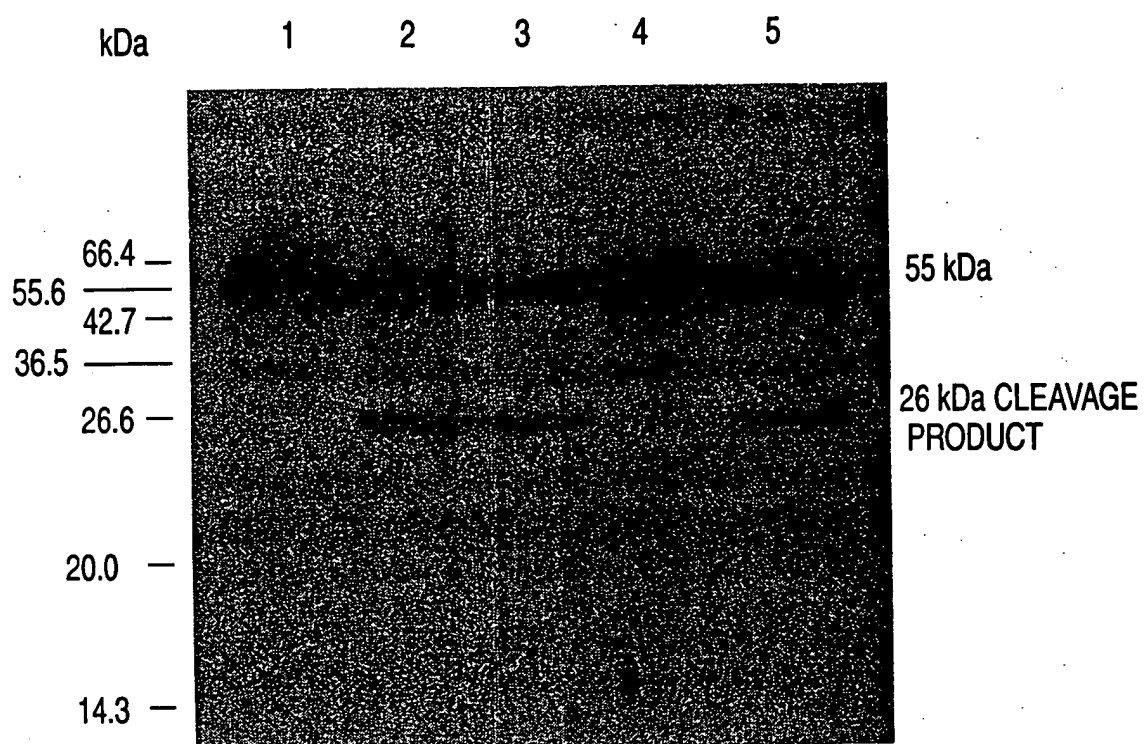


Fig. 13

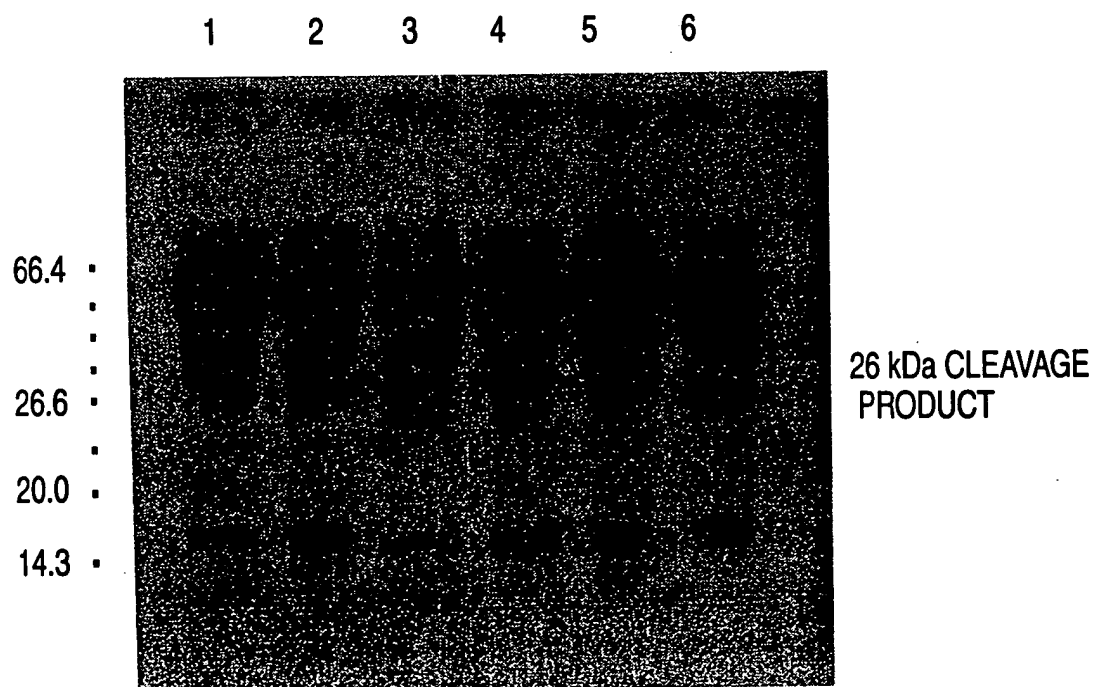
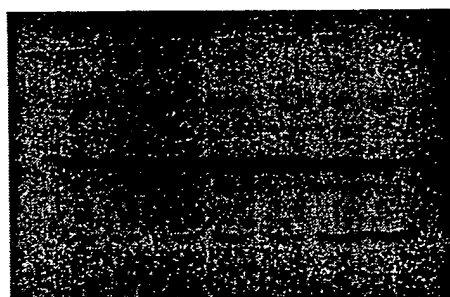


Fig. 14

FOOT " 2051650

**Jurkat**

M 0 1 2 3 5 10 22 (Hours)



-26 kDa

**Fig. 15A**



-26 kDa

**Fig. 15B**

**SECRET**



3 HOURS  
HOURS 0 3 7 Cyto. Nucl.

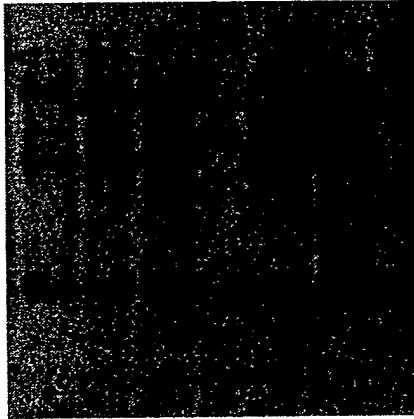
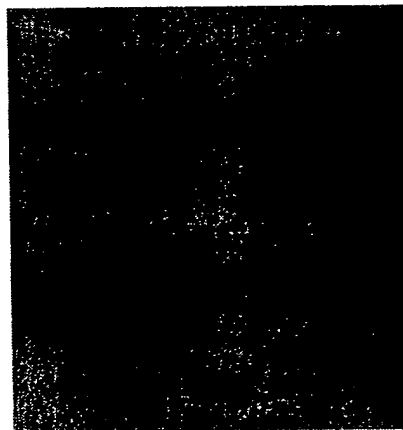


Fig. 16A

3 HOURS  
MARKERS 0 3 7 Cyto. Nucl.

97.2 —  
66.4 —  
55.6 —  
42.7 —  
36.5 —  
26.6 —



← 55 kDa

← 25 kDa

Fig. 16B

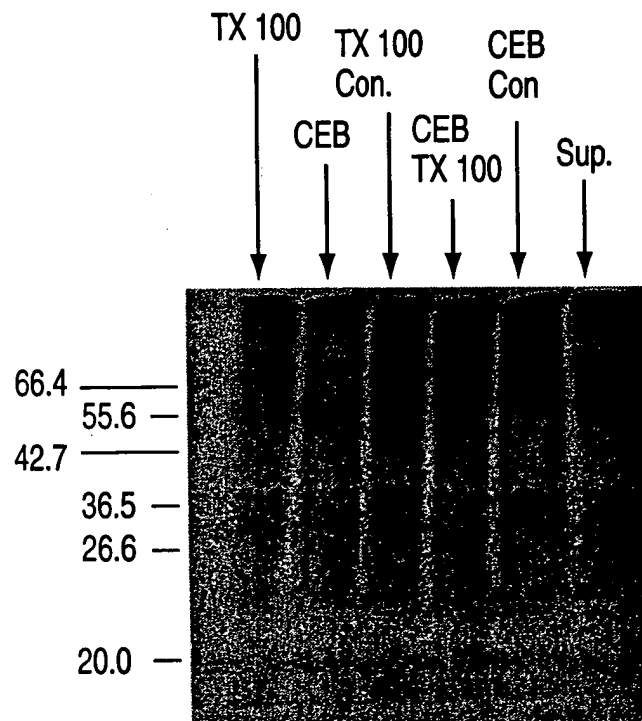


Fig. 17

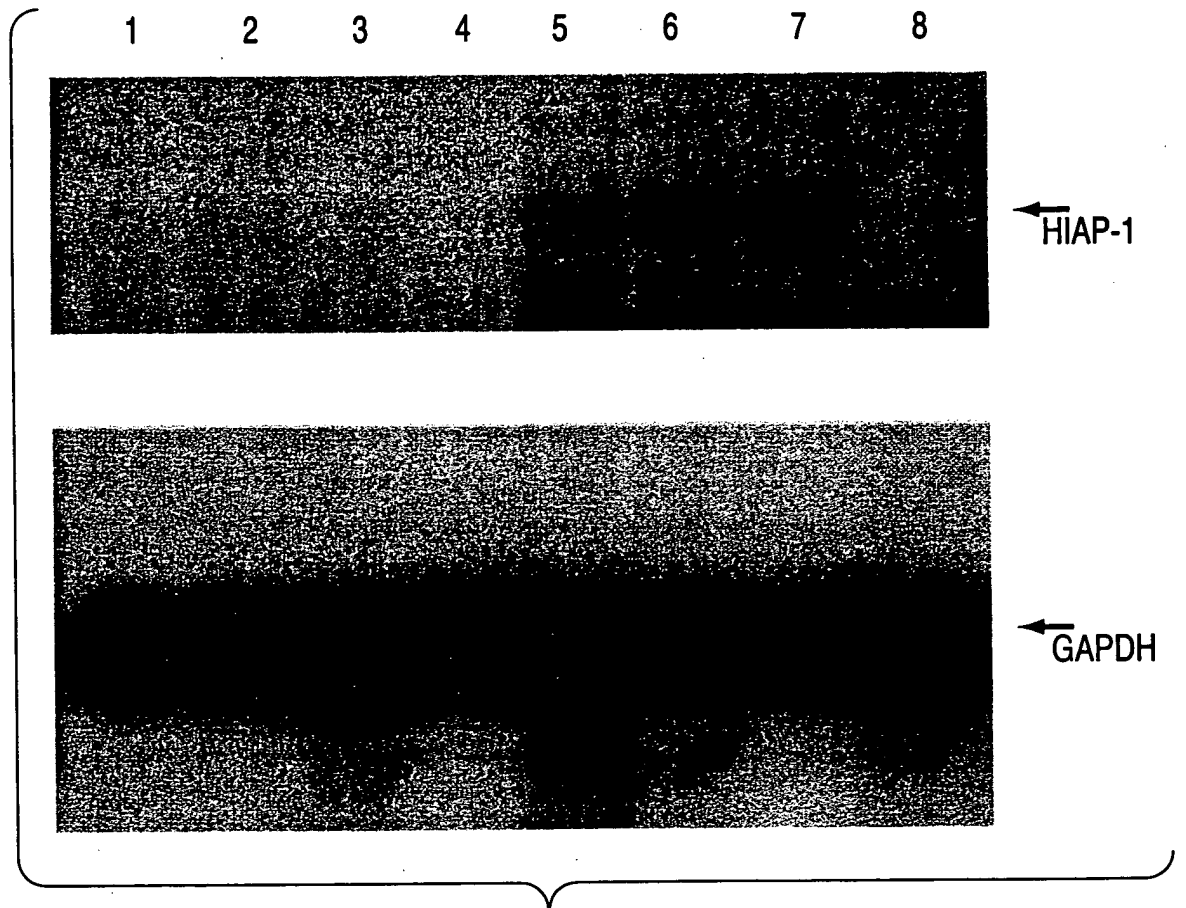
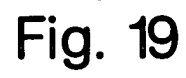


Fig. 18



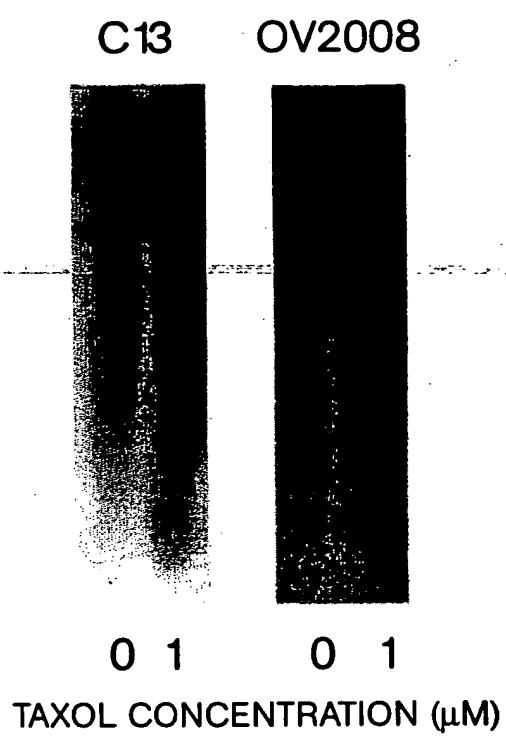


Fig. 20

10001260

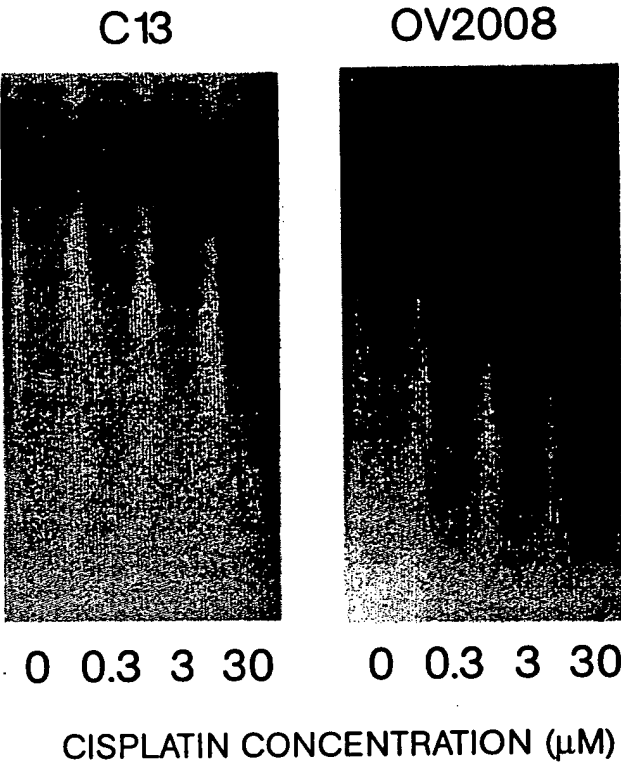


Fig. 21

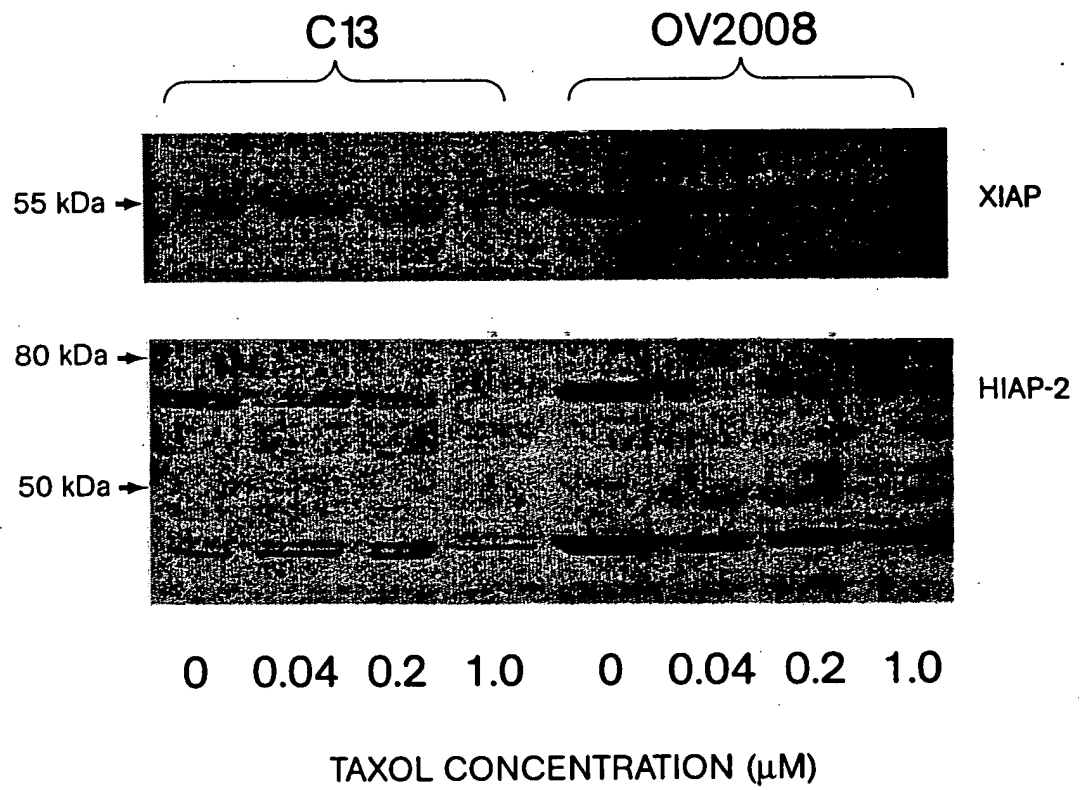


Fig. 22

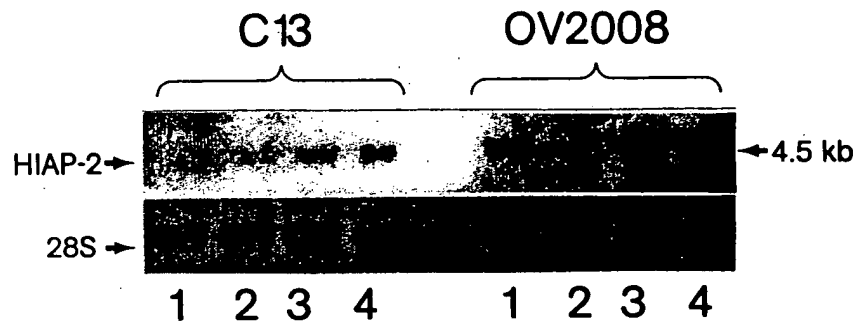


Fig. 23A

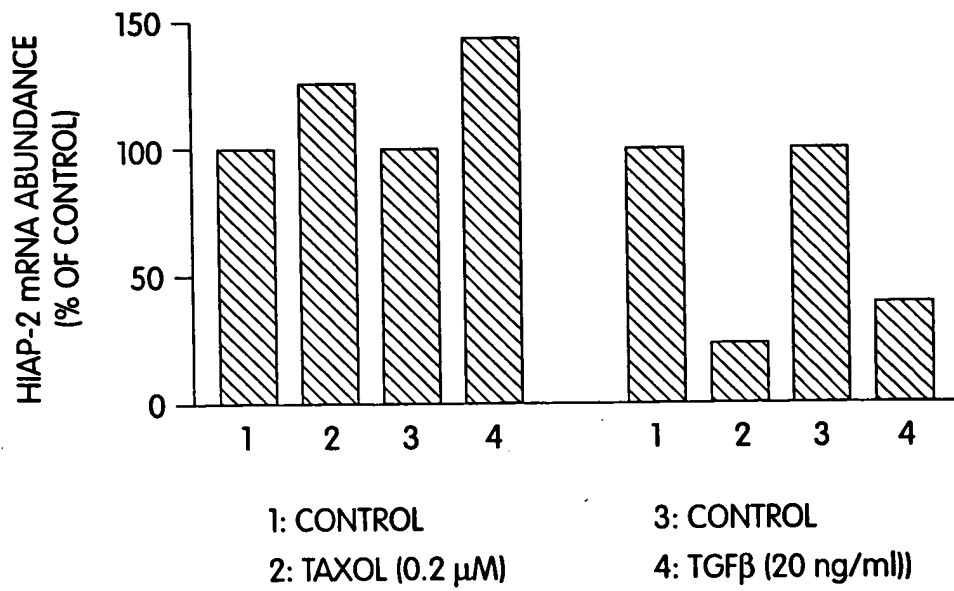


Fig. 23B



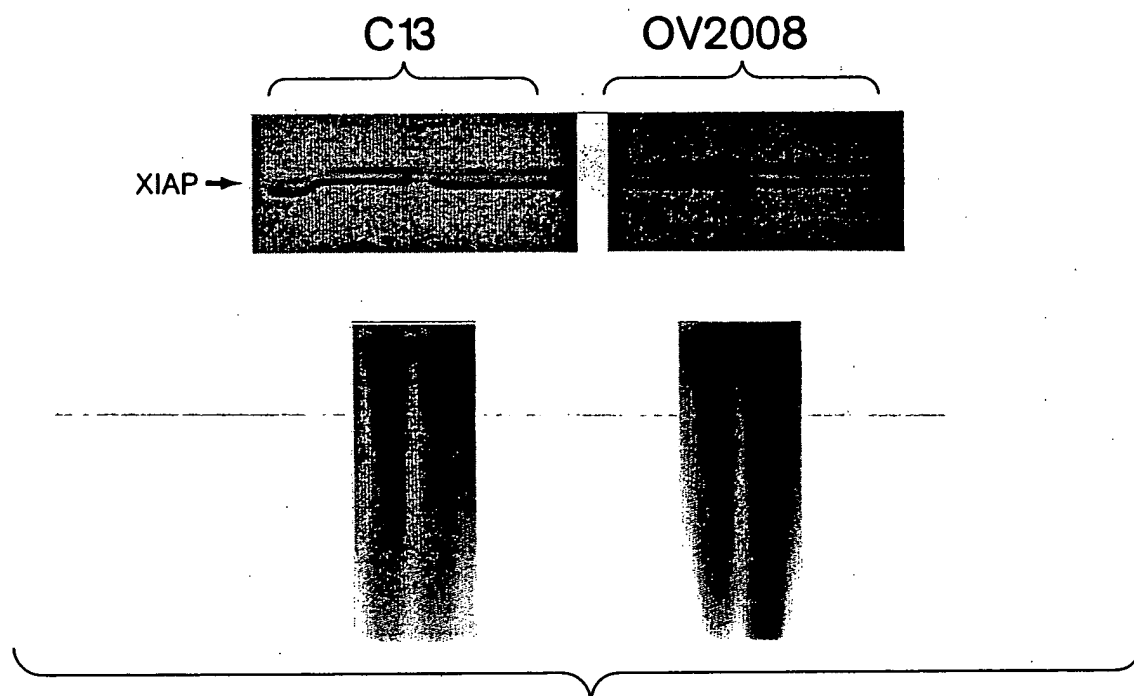


Fig. 24A

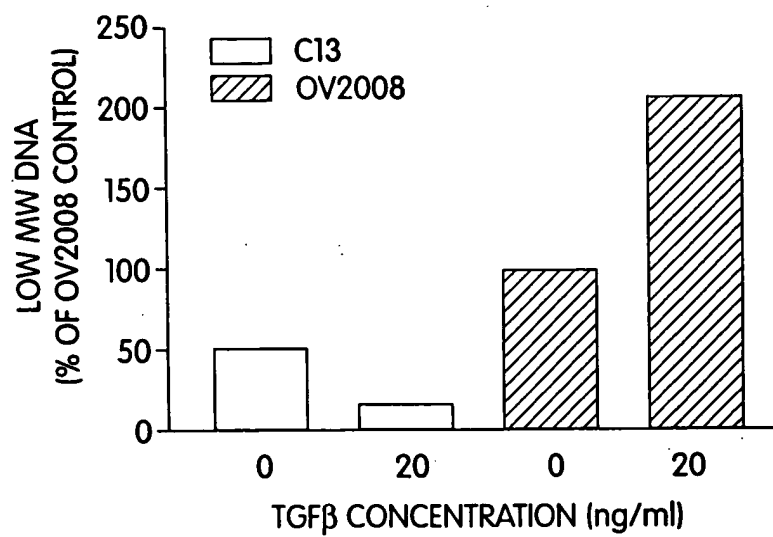


Fig. 24B